

9/18

**Fig. 9**

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

Pig uricase:

Pig cDNA from 1 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

**[GCG GAP program]**

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1493	Length:	305
Ratio:	4.895	Gaps:	0
Percent Similarity:	94.098	Percent Identity:	90.820

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 2
. = 1

```

Pig.pep x baboon D3H.pep

June 25, 1998 17:44 ..

```

Pig  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDQKGYHSIKEVATSVQLT  50
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
Bab  1 MAHYHNNYKKNDELEFVRTGYGKDMVKVLHIQRDQKGYHSIKEVATSVQLT  50
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

51  LSSKKDYLHGDNDSVIPTDTIKNTVNVLAKFRGIKSIETFAVTICEHFLS  100
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
51  LSSKKDYLHGDNDSIIPDTDTIKNTVHVLAKEFRGIKSIETAFGVNICEYFLS  100
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP  150
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
101 SFNHVIRAQVYVEEIPWKRLEKNGVKHVHAFIHTPTGTHFCEVEQLRSGP  150
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLTYDQVLTGQV  250
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
201 QCRDVFDEATWGTIRDLVLEKFAGPYDKGEYSPSVQKTLTYDQVLSLSRV  250
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

251 PEIEDMEISLNPNIHYLNIDMSKMGLINKKEVLLPLDNPYGRITGTVKRKL  300
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.
251 PEIEDMEISLNPNIHYFNIDMSKMGLINKKEVLLPLDNPYGAITGTVKRKL  300
      |||||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.|||.

301 TSRL* 305
      .|||
301 SSRL* 305

```



11/18

**Fig. 11-1**

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. pig uricase

**"Pig KS" uricase:**

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000

Quality:	9036	Length:	915
Ratio:	9.875	Gaps:	0
Percent Similarity:	99.344	Percent Identity:	99.344

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 5
. = 1

```

pigKS.seq x pig.seq July 25, 1998 10:14 ..

```

PKS   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
pig   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50

51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100

101 ATGGAATAATACAGCATTAAAGAGGTGGCAACTTCAGTGCACCTGACT 150
    |||||
101 ATGGAATAATACAGCATTAAAGAGGTGGCAACTTCAGTGCACCTGACT 150

151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
    |||||
151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200

201 TACAGACACCATCAAGAACAAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
    |||||
201 TACAGACACCATCAAGAACAAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250

251 TCAAAAGCATAGAAAACCTTTGCTGTGACTATCTGTGAGCATTTCTCTTCT 300
    |||||
251 TCAAAAGCATAGAAAACCTTTGCTGTGACTATCTGTGAGCATTTCTCTTCT 300

301 TCCTTCAAGCATGTTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
    |||||
301 TCCTTCAAGCATGTTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350

351 GAAGCGTTTGGAAAAGAATGGAGTTAAGCATGTCCATGCATTATTATTTATA 400
    |||||
351 GAAGCGTTTGGAAAAGAATGGAGTTAAGCATGTCCATGCATTATTATTTATA 400

```